Introduction

Two whole blood samples were provided, representing samples from haemoglobinopathy patients referred for genotyping to facilitate transfusion support. Laboratories were requested to undertake red cell genotyping in the same way as for a similar clinical sample, report the method used, and report the genotype and predicted phenotype for D, Cc, Ee, MN, Ss, Kk, Fy^a, Fy^b, Fy, Jk^a, Jk^b, Do^a and Do^b

Return rate / data analysis

The exercise was distributed to 56 laboratories, 13 in the UK and Republic of Ireland (ROI) and 43 outside of the UK. Results were returned by 45/56 (80.4%) laboratories by the closing date.

Results of testing

One laboratory reported unsatisfactory sample quality for both patient samples, citing haemolysis.

Five laboratories returned results that were outwith consensus and these are highlighted in Table 1.

Table 1 - Results outwith consensus

Laboratory	Patient sample	Reported Genotype	Consensus genotype	Reported predicted phenotype	Consensus predicted phenotype
A	Patient 1	*KEL*01/02*	*KEL*01/01*	K+ k+	K+ k-
		*FY*02/02* GATA mutation not present	*FY*01/02* GATA mutation not present	Fy(a-b+)	Fy(a+b+)
		*JK*01/02*	*JK*02/02*	Jk(a+b+)	Jk(a-b+)
	Patient 2	*KEL*01/01*	*KEL*01/02*	K+ k-	K+ k+
		*FY*01/02* GATA mutation not present	*FY*02/02* GATA mutation not present	Fy(a+b+)	Fy(a-b+)
		*JK*02/02*	*JK*01/02*	Jk(a-b+)	Jk(a+b+)
B	Patient 1	*GYPB*03/04*	*GYPB*04/04*	S+ s+	S- s+
		*KEL*02/02*	*KEL*01/01*	K- k+	K+ k-
		*FY*01/01* GATA mutation not tested	*FY*01/02* GATA mutation not present	Fy(a+b-)	Fy(a+b+)
		*JK*01/02*	*JK*02/02*	Jk(a+b+)	Jk(a-b+)
		*DO*02/02*	*DO*01/02*	Do(a-b+)	Do(a+b+)
C	Patient 1	*FY*02/02* GATA mutation not present	*FY*01/02* GATA mutation not present	Fy(a-b+)	Fy(a+b+)
D	Patient 1	*FY*02/02* GATA mutation not present	*FY*01/02* GATA mutation not present	Fy(a-b+)	Fy(a+b+)
E	Patient 1	*RHD*01/01N.01*	*RHD*01N.01/01N.01*	D negative	D negative
	Patient 2	*RHD*01/01N.01*	*RHD*01N.01/01N.01*	D negative	D negative

Discussion

Laboratory A appear to have transposed either samples or results for Patient 1 and 2 resulting in six incorrect genotypes and six incorrect corresponding predicted phenotypes. Laboratory E, presumably making a data entry error recorded incorrect *RHD*01* genotypes for both patients, but recorded correct predicted phenotypes.

Care should be taken to confirm the identity of all samples before testing. For clinical samples, this requires a full check of the patient demographic details to ensure that results are assigned to the correct patient. EQA samples should be subject to the same process with a check of the patient number and exercise code on each sample.

Of those answering the question, 22/43 (51.2%) of laboratories indicated that their results were either transcribed manually to a paper report or transcribed manually to an IT system. When entering data for EQA samples it is important to check that the data is being recorded and transcribed against the correct patient and this also applies to manual data entry or transcription of results of clinical samples.

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Your results for Patient 1

Result(s) outwith consensus? : No

Your results for Patient 1, compared to consensus results

Consensus results		Antigens	Your results				
Genotype	Predicted phenotype[1]		Genotype	Specify 'other' genotype	Predicted phenotype	Specify 'other' phenotype	Other terminology reported to clinicians
*RHD*01N.01/01N.01*	D negative	D	*RHD*01N.01/01N.01*		D negative		
*RHCE*c/c*	C- c+	CcEe	*RHCE*c/c*		C- c+		ccee
*RHCE*e/e*	E- e+	CcEe	*RHCE*e/e*		E- e+		
*GYPA*01/02*	M+ N+	MN	*GYPA*01/02*		M+ N+		MN
*GYPB*04/04*	S- s+	Ss	*GYPB*04/04*		S- s+		ss
*KEL*01/01*	K+ k-	Kk	*KEL*01/01*		K+ k-		KK
*FY*01/02* GATA mutation not present	Fy(a+b+)	Fy^a Fy^b Fy	*FY*01/02* GATA mutation not present		Fy(a+b+)		
*JK*02/02*	Jk(a-b+)	Jk^a Jk^b	*JK*02/02*		Jk(a-b+)		
*DO*01/02*	Do(a+b+)	Do^a Do^b	*DO*01/02*		Do(a+b+)		

Your results for Patient 2

Result(s) outwith consensus? : No

Your results for Patient 2, compared to consensus results

Consensus results		Antigens	Your results				
Genotype	Predicted phenotype[1]		Genotype	Specify 'other' genotype	Predicted phenotype	Specify 'other' phenotype	Other terminology reported to clinicians
*RHD*01N.01/01N.01*	D negative	D	*RHD*01N.01/01N.01*		D negative		
*RHCE*c/c*	C- c+	CcEe	*RHCE*c/c*		C- c+		ccee
*RHCE*e/e*	E- e+	CcEe	*RHCE*e/e*		E- e+		
*GYPA*01/02*	M+ N+	MN	*GYPA*01/02*		M+ N+		MN
*GYPB*04/04*	S- s+	Ss	*GYPB*04/04*		S- s+		ss
*KEL*01/02*	K+ k+	Kk	*KEL*01/02*		K+ k+		Kk
*FY*02/02* GATA mutation not present	Fy(a-b+)	Fy^a Fy^b Fy	*FY*02/02* GATA mutation not present		Fy(a-b+)		
*JK*01/02*	Jk(a+b+)	Jk^a Jk^b	*JK*01/02*		Jk(a+b+)		
*DO*01/02*	Do(a+b+)	Do^a Do^b	*DO*01/02*		Do(a+b+)		